

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Le, Junming
 Vilcek, Jan
 Daddona, Peter E.
 Ghrayeb, John
 Knight, David M.
 Siegel, Scott A.
- (ii) TITLE OF INVENTION: MONOCLONAL AND CHIMERIC ANTIBODIES
 SPECIFIC FOR HUMAN TUMOR NECROSIS FACTOR
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Browdy and Neimark
 (B) STREET: 419 Seventh Street, N.W.
 (C) CITY: Washington
 (D) STATE: D.C.
 (E) COUNTRY: USA
 (F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0,
 Version #1.25
- (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: US 07/670,827
 (B) FILING DATE: 18-MAR-1991
- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 202-628-5197
 (B) TELEFAX: 202-737-3528

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ser | Ser | Ser | Arg | Thr | Pro | Ser | Asp | Lys | Pro | Val | Ala | His | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ala | Asn | Pro | Gln | Ala | Glu | Gly | Gln | Leu | Gln | Trp | Leu | Asn | Arg | Arg |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ala | Asn | Ala | Leu | Leu | Ala | Asn | Gly | Val | Glu | Leu | Arg | Asp | Asn | Gln | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

5 Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

10 Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..321

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAC ATC TTG CTG ACT CAG TCT CCA GCC ATC CTG TCT GTG AGT CCA GGA 48
Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

30 GAA AGA GTC AGT TTC TCC TGC AGG GCC AGT CAG TTC GTT GGC TCA AGC 96
Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

ATC CAC TGG TAT CAG CAA AGA ACA AAT GGT TCT CCA AGG CTT CTC ATA 144
Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

35 AAG TAT GCT TCT GAG TCT ATG TCT GGG ATC CCT TCC AGG TTT AGT GGC 192
Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

40 AGT GGA TCA GGG ACA GAT TTT ACT CTT AGC ATC AAC ACT GTG GAG TCT 240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80

GAA GAT ATT GCA GAT TAT TAC TGT CAA CAA AGT CAT AGC TGG CCA TTC 288
Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

ACG TTC GGC TCG GGG ACA AAT TTG GAA GTA AAA
 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
 100 105

321

(2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
 1 5 10 15
 Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
 20 25 30
 15 Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
 35 40 45
 Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60
 20 Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
 65 70 75 80
 Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
 85 90 95
 Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys
 100 105

25 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..357

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAA GTG AAG CTT GAG GAG TCT GGA GGA GGC TTG GTG CAA CCT GGA GGA 48
 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 TCC ATG AAA CTC TCC TGT GTT GCC TCT GGA TTC ATT TTC AGT AAC CAC 96
 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
 20 25 30

	TGG	ATG	AAC	TGG	GTC	CGC	CAG	TCT	CCA	GAG	AAG	GGG	CTT	GAG	TGG	GTT	144
	Trp	Met	Asn	Trp	Val	Arg	Gln	Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val	
			35					40					45				
5	GCT	GAA	ATT	AGA	TCA	AAA	TCT	ATT	AAT	TCT	GCA	ACA	CAT	TAT	GCG	GAG	192
	Ala	Glu	Ile	Arg	Ser	Lys	Ser	Ile	Asn	Ser	Ala	Thr	His	Tyr	Ala	Glu	
		50					55				60						
	TCT	GTG	AAA	GGG	AGG	TTC	ACC	ATC	TCA	AGA	GAT	GAT	TCC	AAA	AGT	GCT	240
	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ala	
		65				70					75					80	
10	GTC	TAC	CTG	CAA	ATG	ACC	GAC	TTA	AGA	ACT	GAA	GAC	ACT	GGC	GTT	TAT	288
	Val	Tyr	Leu	Gln	Met	Thr	Asp	Leu	Arg	Thr	Glu	Asp	Thr	Gly	Val	Tyr	
					85					90					95		
	TAC	TGT	TCC	AGG	AAT	TAC	TAC	GGT	AGT	ACC	TAC	GAC	TAC	TGG	GGC	CAA	336
15	Tyr	Cys	Ser	Arg	Asn	Tyr	Tyr	Gly	Ser	Thr	Tyr	Asp	Tyr	Trp	Gly	Gln	
				100					105					110			
	GGC	ACC	ACT	CTC	ACA	GTC	TCC										357
	Gly	Thr	Thr	Leu	Thr	Val	Ser										
				115													

(2) INFORMATION FOR SEQ ID NO:5:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Glu	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
	1				5					10					15		
	Ser	Met	Lys	Leu	Ser	Cys	Val	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Asn	His	
				20					25					30			
30	Trp	Met	Asn	Trp	Val	Arg	Gln	Ser	Pro	Glu	Lys	Gly	Leu	Glu	Trp	Val	
			35				40						45				
	Ala	Glu	Ile	Arg	Ser	Lys	Ser	Ile	Asn	Ser	Ala	Thr	His	Tyr	Ala	Glu	
		50					55				60						
35	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Ser	Ala	
		65				70				75					80		
	Val	Tyr	Leu	Gln	Met	Thr	Asp	Leu	Arg	Thr	Glu	Asp	Thr	Gly	Val	Tyr	
					85				90						95		
	Tyr	Cys	Ser	Arg	Asn	Tyr	Tyr	Gly	Ser	Thr	Tyr	Asp	Tyr	Trp	Gly	Gln	
				100					105					110			
40	Gly	Thr	Thr	Leu	Thr	Val	Ser										
				115													